

FIGURE 1

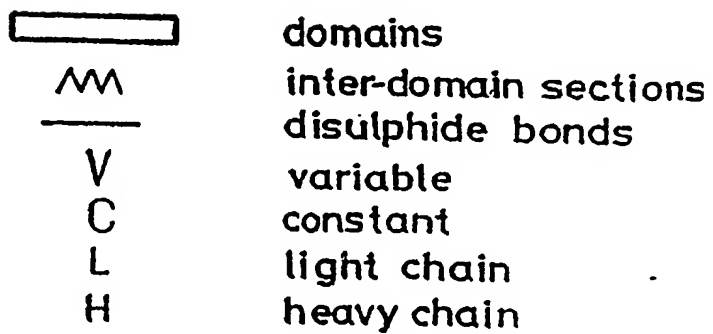
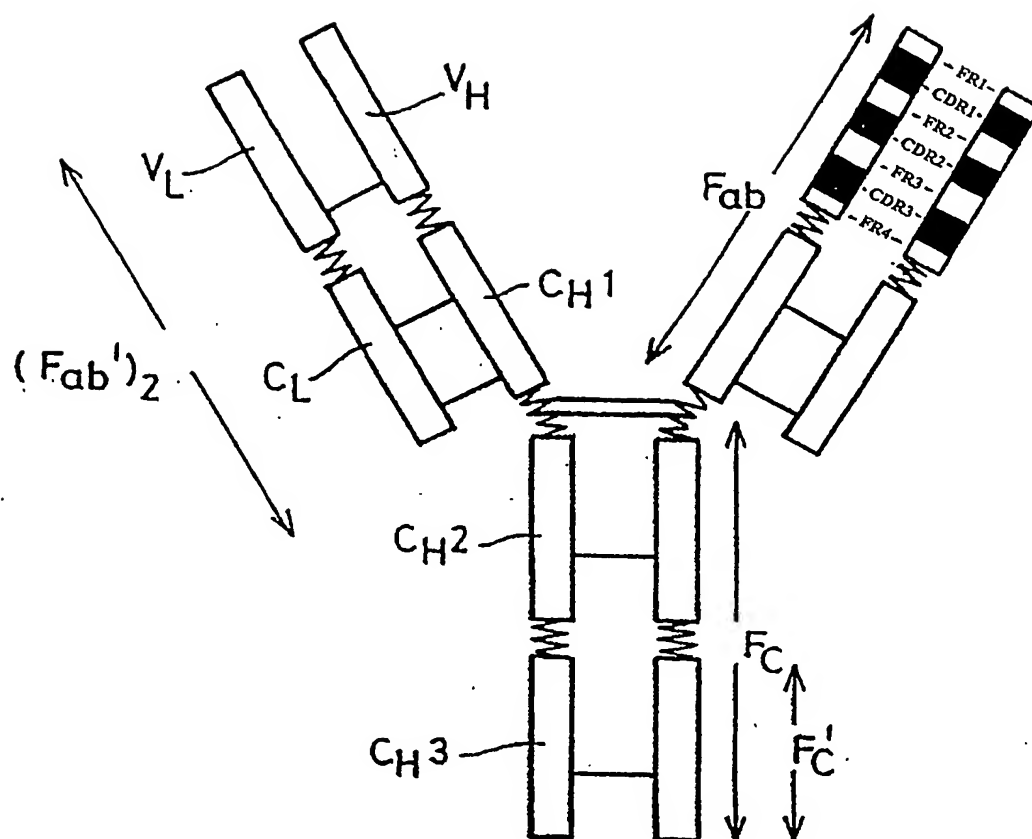


FIGURE 2**A.****SEQ ID NO:59 - AME 33 light chain variable region amino acid sequence**

EIVLTQSPGTLSPGERATLSCRASSVPYIHWYQQKPGQAPRLLIYATSALASGI
PDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQWLSNPPTFGQGTKLEIK

B.**SEQ ID NO:60 - AME 33 light chain variable region nucleic acid sequence**

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAG
AGCCACCCTCTCCTGCAGGGCCAGCTCAAGTGTACCGTACATCCACTGGTAC
CAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGCCACATCCGCTCT
GGCTTCTGGCATCCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGACAGACTTC
ACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCA
GCAGTGGCTGAGTAACCCACCCACTTTTGGCCAGGGGACCAAGCTGGAGATC
AAA

FIGURE 3**A.****SEQ ID NO:61 - AME 33 heavy chain variable region amino acid sequence**

EVQLVQSGAEVKKPGESLKISCKGSGRTFTSYNMHWVRQMPGKGLEWMGAIYP
LTGDTSYNQKSKLQVTISADKSISTAYLQWSSLKASDTAMY YCARSTYVGGDW
QFDVWGKGTTVTVSS

B.**SEQ ID NO:62 - AME 33 heavy chain variable region nucleic acid sequence**

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCT
CTGAAGATCTCCTGTAAGGGTTCTGGCCGTACATTTACCAGTTACAATATGCA
CTGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGGGCTATTTAT
CCCTTGACGGGTGATACTTCCTACAATCAGAAGTCGAAACTCCAGGTCACCA
TCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAA
GGCCTCGGACACCGCCATGTATTACTGTGCGAGATCGACTTACGTGGGCGGT
GACTGGCAGTTCGATGTCTGGGGCAAGGGGACCACGGTCACCGTCTCCTCA

FIGURE 4**A. Amino acid sequence of a human light chain framework region VkIII (A27) (DPK22) with interspersed CDR sequences labeled**

(FRL1 - SEQ ID NO:71) CDRL1 (FRL2 - SEQ ID NO:72) CDRL2
 EIVLTQSPGTL~~SLSPGERATLSC~~XXXXXXXXXXXXWYQQKPGQAPRLLIYXXXXXXXXXX
 (FRL3 - SEQ ID NO:73) CDRL3 (FRL4 - SEQ ID NO:74)
 GIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCXXXXXXXXXXXXFGQGTKLEIK

B. Nucleic acid sequence of a human light chain framework region VkIII (A27) (DPK22) with interspersed CDR sequences labeled

(FRL1 - SEQ ID NO:75)
 GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAG
 CDRL1
 CCACCCTCTCCTGCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTGGTACCAG
 (FRL2 - SEQ ID NO:76) CDRL2
 CAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATXXXXXXXXXXXXXXXXXXXX
XXXGGCATCCCAGACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTC
 (FRL3 - SEQ ID NO:77)
 ACCATCAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTXXXXXXXXXX
 CDRL3 (FRL4 - SEQ ID NO:78)
XXXXXXXXXXXXXXXXXXXXTTTGGCCAGGGGACCAAGCTGGAGATCAAA

FIGURE 5**A. Amino acid sequence of a human heavy chain framework region VH5-51
(DP-73) with interspersed CDR sequences labeled**

(FRH1 - SEQ ID NO:79) CDRH1 (FRH2 - SEQ ID NO:80)
 EVQLVQSGAEVKKPGESLKISCKGSXXXXXXXXXXWVRQMPGKGLEWMG

CDRH2 (FRH3 - SEQ ID NO:81)
 XXXXXXXXXXXXXXXXXXXXQVTISADKSISTAYLQWSSLKASDTAMYYCAR

CDRH3 (FRH4 - SEQ ID NO:82)
 XXXXXXXXXXXXXXXWGKGTTVTVSS

**B. Nucleic acid sequence of a human heavy chain framework region VH5-51
(DP-73) with interspersed CDR sequences labeled**

(FRH1 - SEQ ID NO:83)
 GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTG

CDRH1
 AAGATCTCCTGTAAGGGTTCTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

(FRH2 - SEQ ID NO:84)
 TGGGTGCGCCAGATGCCCCGGGAAAGGCCTGGAGTGGATGGGG

CDRH2
 XXX

CAGGTCACCATCTCAGCCGACAAGTCCATCAGCACCGCCTACCTGCAGTGGAGC

(FRH3 - SEQ ID NO:85)
 AGCCTGAAGGCCTCGGACACCGCCATGTATTACTGTGCGAGAXXXXXXXXXXX

CDRH3 (FRH4 - SEQ ID NO:86)
 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXTGGGGCAAGGGGACCACGGTCACCGTCT

CCTCA

FIGURE 6**A.****SEQ ID NO:63 - AME 5 light chain variable region amino acid sequence**

DIQMTQSPSSLSASVGDRVTITCRASSSVHYIHWYQQKPGKVPKLLIYATSGLAS
GVPSRFSGSGSGTDFTLTISLQPEDVATYYCQWTWTFNPPTFGGGTKVEIK

B.**SEQ ID NO:64 - AME 5 light chain variable region nucleic acid sequence**

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGA
GACAGAGTCACCATCACTTGCAGGGCCAGCTCAAGTGTACATTACATC
CACTGGTACCAGCAGAAACCAGGGAAAGTTCCTAAGCTCTTGATCTAT
GCCACATCCGGCCTGGCTTCTGGGGTCCCATCTCGGTTCAAGTGGCAGT
GGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAA
GATGTTGCCACTTATTACTGCCAGACTTGGACTTTTAACCCTCCCACG
TTCGGCGGAGGGACCAAGGTGGAGATCAAA

FIGURE 7**A.****SEQ ID NO:65 - AME 5 heavy chain variable region amino acid sequence**

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYNMHWVRQAPGQGLEWMGAIY
PGNGDTSYNQKFKWRVTMTRDTSTSTVYMELSSLRSEDTAVYYCARSTYYGGD
WQFDEWGKGTTVTVSS

B.**SEQ ID NO:66 - AME 5 heavy chain variable region nucleic acid sequence**

CAGGTGCAGCTGGTGCAGTCTGGTGCTGAAGTGAAGAAGCCTGGGGCC
TCAGTGAAGGTGTCCTGCAAGGCATCTGGATACACCTTCACCAGCTAC
AATATGCACTGGGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATG
GGAGCCATCTATCCTGGAAATGGTGATACAAGCTACAATCAGAAGTTT
AAATGGAGAGTCACCATGACCAGGGACACGTCCACGAGCACAGTCTAC
ATGGAGCTGAGCAGCCTGAGATCTGAGGACACGGCCGTGTATTACTGT
GCGAGATCGACTTATTACGGCGGTGACTGGCAGTTCGACGAGTGGGGC
AAAGGGACCACGGTCACCGTCTCCTCA

FIGURE 8**A. Amino acid sequence of a human light chain framework region VkI (DPK4) (A20) with interspersed CDR sequences labeled**

(FRL1 - SEQ ID NO:87) (CDRL1) (FRL2 - SEQ ID NO:88) (CDRL2)
 DIQMTQSPSSLSASVGDRVTITCXXXXXXXXXXWYQQKPGKVPKLLIYXXXXXXXX
 (FRL3 - SEQ ID NO:89) (CDRL3) (FRL4 - SEQ ID NO:90)
 GVPSRFSGSGSGTDFTLTISSLQPEDVATYYCXXXXXXXXXXFGGGTKVEIK

B. Nucleic acid sequence of a human light chain framework region VkI (DPK4) (A20) with interspersed CDR sequences labeled

(FRL1 - SEQ ID NO:91)
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAG
 (CDRL1)
 TCACCATCACTTGCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTTGGTACCAG
 (FRL2 - SEQ ID NO:92) (CDRL2)
 CAGAAACCAGGGGAAAGTTCCTAAGCTCTTGATCTATXXXXXXXXXXXXXXXXXXXX
 (CDRL2 cont.) (FRL3 - SEQ ID NO:93)
 XXXXGGGGTCCCATCTCGGTTCAAGTGGCAGTGGATCTGGGACAGATTTCACTCT
 CACCATCAGCAGCCTGCAGCCTGAAGATGTTGCCACTTATTACTGCXXXXXXXX
 (CDRL3) (FRL4 - SEQ ID NO:94)
 XXXXXXXXXXXXXXXXXXXXXTTCGGCGGAGGGACCAAGGTGGAGA

TCAAA

FIGURE 9**A. Amino acid sequence of a human heavy chain framework region VHI DP7/21-2 with interspersed CDR sequences labeled**

(FRH1 - SEQ ID NO:95) (CDRH1) (FRH2 - SEQ ID NO:96)
 QVQLVQSGAEVKKPGASVKVSCKASXXXXXXXXXXXXWVRQAPGQGLEWMG
 (CDRH2) (FRH3 - SEQ ID NO:97)
 XXXXXXXXXXXXXXXXXXXXXRVTMTRDTSTSTVYMELSSLRSEDTAVYYCAR
 (CDRH3) (FRH4 - SEQ ID NO:98)
 XXXXXXXXXXXXXXXWGKGTTVTVSS

B. Nucleic acid sequence of a human heavy chain framework region VHI DP7/21-2 with interspersed CDR sequences labeled

(FRH1 - SEQ ID NO:99)
 CAGGTGCAGCTGGTGCAGTCTGGTGCTGAAGTGAAGAAGCCTGGGGCCTCAGTG
 (CDRH1)
 AAGGTGTCCTGCAAGGCATCTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
 (FRH2 - SEQ ID NO:100) (CDRH2)
 GGTGCGACAGGCCCTGGACAAGGGCTTGAGTGGATGGGAXXXXXXXXXXXXX
 (CDRH2 cont.)
 XXAGAGTCACCATGAC
 (FRH3 - SEQ ID NO:101)
 CAGGGACACGTCCACGAGCACAGTCTACATGGAGCTGAGCAGCCTGAGATCTGA
 (CDRH3)
 GGACACGGCCGTGTATTACTGTGCGAGAXXXXXXXXXXXXXXXXXXXXXXXXXX
 (CDRH3) (FRH4 - SEQ ID NO:102)
 XXXXXXXXXXXX
 TGGGGCAAAGGGACCACGGTCACCGTCTCCTCA

FIGURE 10**A.****SEQ ID NO:67 - AME 33 complete light chain amino acid sequence**

EIVLTQSPGTL~~SLSPGERATL~~SCRASSSVPYIHWYQQKPGQAPRLLIYATSALASGIPDR
FSGSGSGTDFTLTISRLEPEDFAVYYCQQWLSNPPTFGQGTKLEIKRTVAAPSVFIFPPS
DEOLKSGTASVCLLNNFYPREAKVQWKVDNALOSGNSQESVTEODSKDSTYSLSST
LTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC

- Constant Region is underlined

B.**SEQ ID NO:68 - AME 33 complete light chain nucleic acid sequence**

GAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAAAGAG
CCACCCTCTCCTGCAGGGCCAGCTCAAGTGTACCGTACATCCACTGGTACCAGCA
GAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGCCACATCCGCTCTGGCTTCTG
GCATCCCAGACAGGTTCAAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACCAT
CAGCAGACTGGAGCCTGAAGATTTTGCAGTGTATTACTGTCAGCAGTGGCTGAGT
AACCCACCCACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAACTGTGGCTG
CACCATCTGTCTTCATCTTCCC GCCATCTGATGAGCAGTTGAAATCTGGAAGTACC
TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGA
AGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGA
CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGA
CTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCG
CCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAG

FIGURE 11**A. SEQ ID NO:69 - AME 33 complete heavy chain amino acid sequence**

EVQLVQSGAEVKKPGESLKISCKGSGRTFTSYNMHWVRQMPGKGLEWMGAIYPLTG
 DTSYNQKSKLQVTISADKSISTAYLQWSSLKASDTAMYYCARSTYVGGDWQFDVWG
 KGTTVTVSS**ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSG**
VHTFPAVLOSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH
TCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGV
EVHNAKTKPREEQYNSTYRVVSVLTVLHODWLNQKEYKCKVSNKALPAPIEKTISKA
KGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTTPV
LDSDGSFFLYSKLTVDKSRWQOGNVFSCSVMEALHNHYTQKSLSLSPGK

- Constant Region is underlined; the "D" at position 280 and "K" at position 290 are in bold

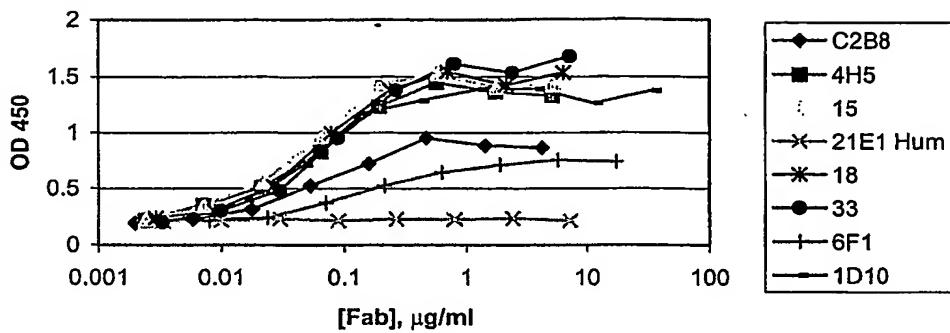
B. SEQ ID NO:70 - AME 33 complete heavy chain nucleic acid sequence

GAGGTGCAGCTGGTGCAGTCTGGAGCAGAGGTGAAAAAGCCCGGGGAGTCTCTG
 AAGATCTCCTGTAAGGGTTCTGGCCGTACATTTACCAGTTACAATATGCACTGGGT
 GCGCCAGATGCCCGGGAAGGCCTGGAGTGGATGGGGGCTATTTATCCCTTGACG
 GGTGATACTTCTACAATCAGAAAGTCGAAACTCCAGGTCACCATCTCAGCCGACA
 AGTCCATCAGCACCGCCTACCTGCAGTGGAGCAGCCTGAAGGCCTCGGACACCGC
 CATGTATTACTGTGCGAGATCGACTTACGTGGGCGGTGACTGGCAGTTCGATGTCT
 GGGGCAAGGGGACCACGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGT
 CTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCT
 GCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCAAGGCGC
 CCTGACCAGCGGCGTGACACCTTCCCCGGCTGTCTACAGTCCTCAGGACTCTACT
 CCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACAT
 CTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAGGTTGAGCC
 CAAATCTTGTGACAAACTCACACATGCCACCGTGCCAGCACCTGAACTCCTG
 GGGGACCGTCAGTCTTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTC
 CCGGACCCCTGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAG
 GTCAAGTTCAACTGGTACGTGGACGGCGTGAGGTGCATAATGCCAAGACAAAG
 CCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGCGTCCTACCGTCC
 TGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAG
 CCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAGGCCAAAGGGCAGCCCCGAGA
 ACCACAGGTGTACACCCTGCCCCCATCCCGGACGAGCTGACCAAGAACCAGGTC
 AGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGG
 AGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTC
 CGACGGCTCCTTCTTCTCTATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAG
 CAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACA
 CGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA

FIGURE 12

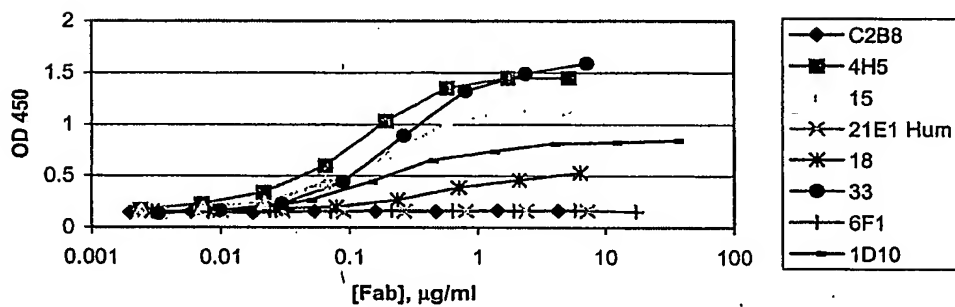
A.

Fab, Binding



B.

Fab, Off rate



C.

Fab, On rate

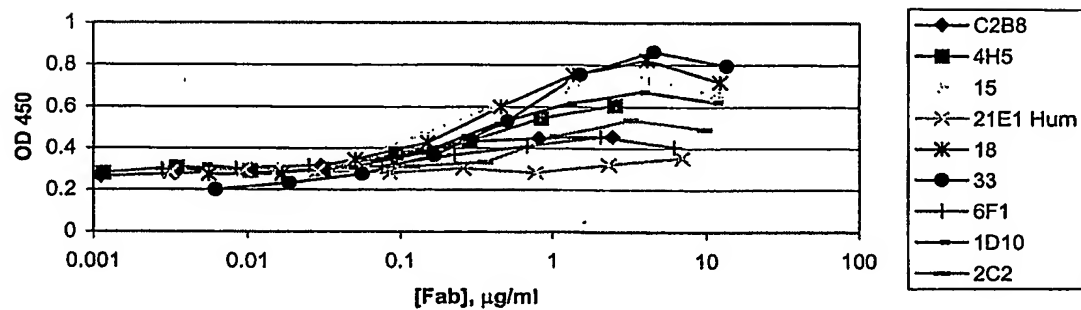
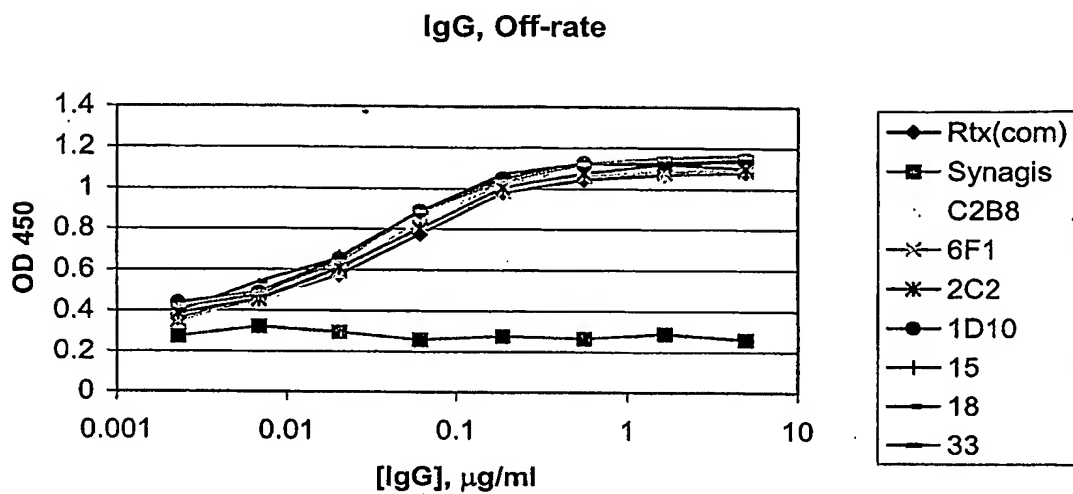


FIGURE 13

A.



B.

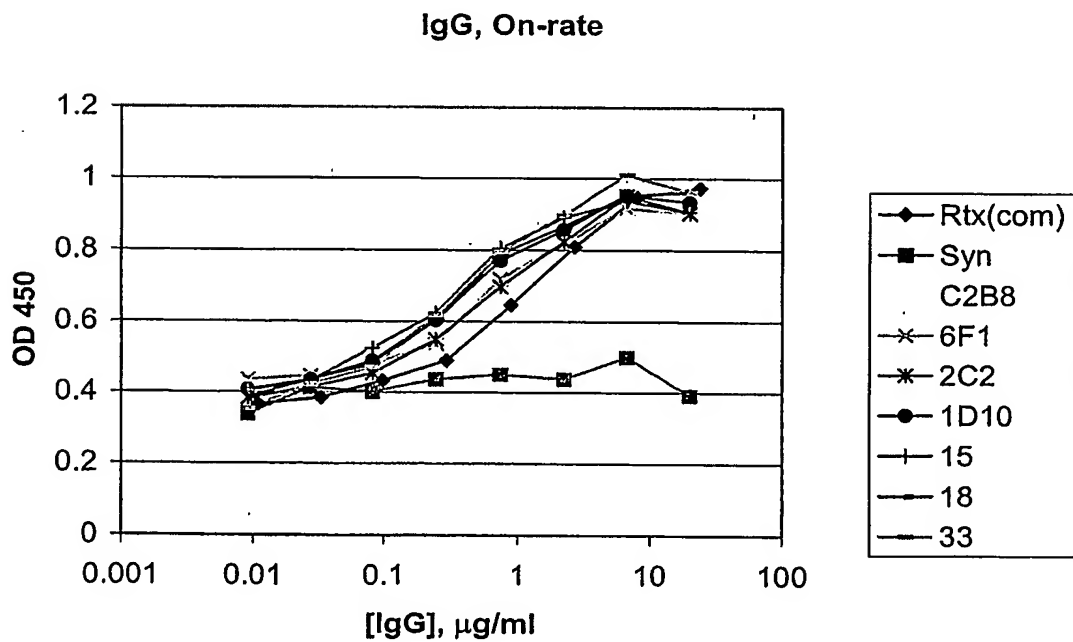
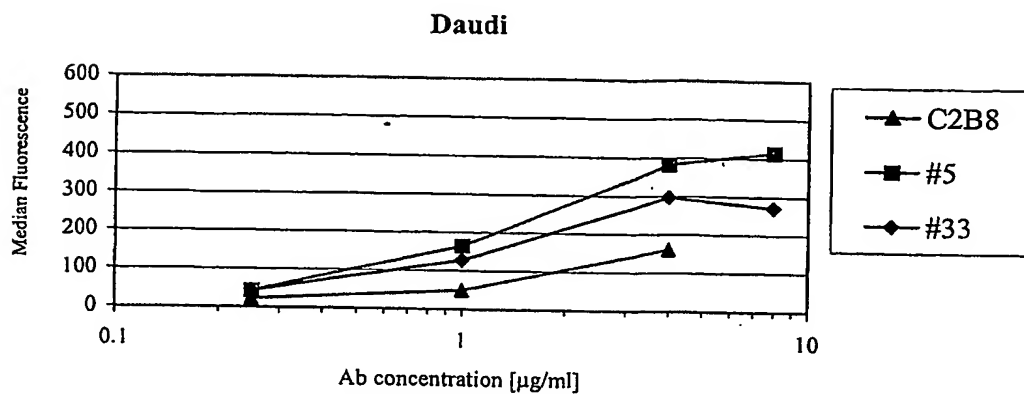
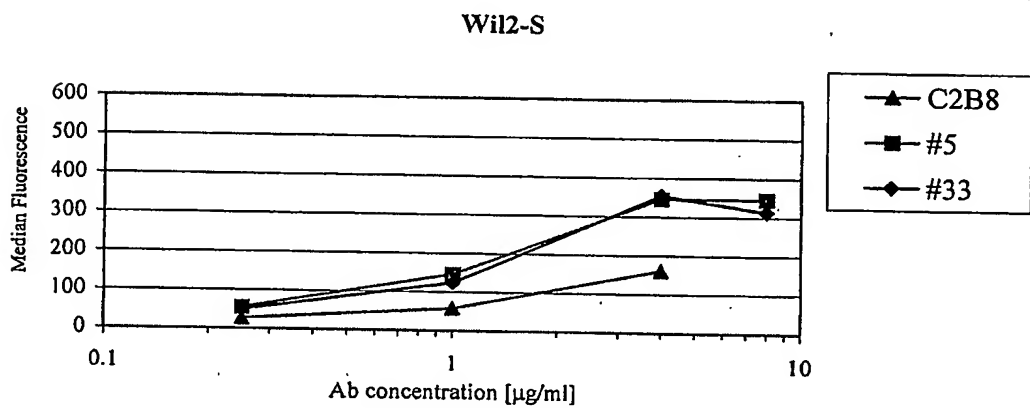


FIGURE 14

A.



B.



C.

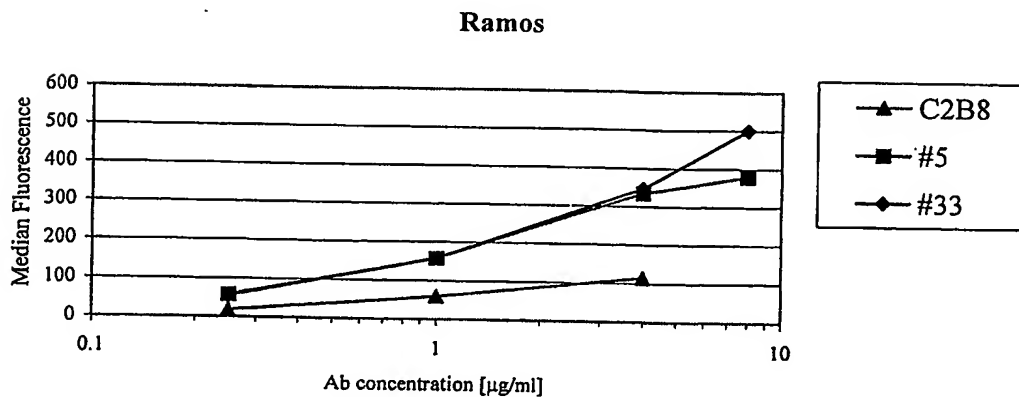


FIGURE 15

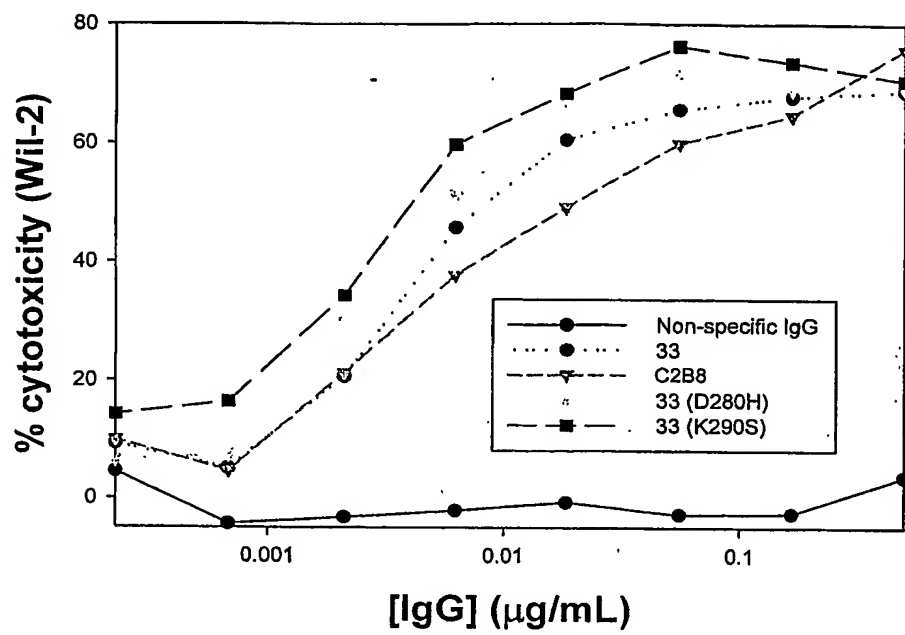
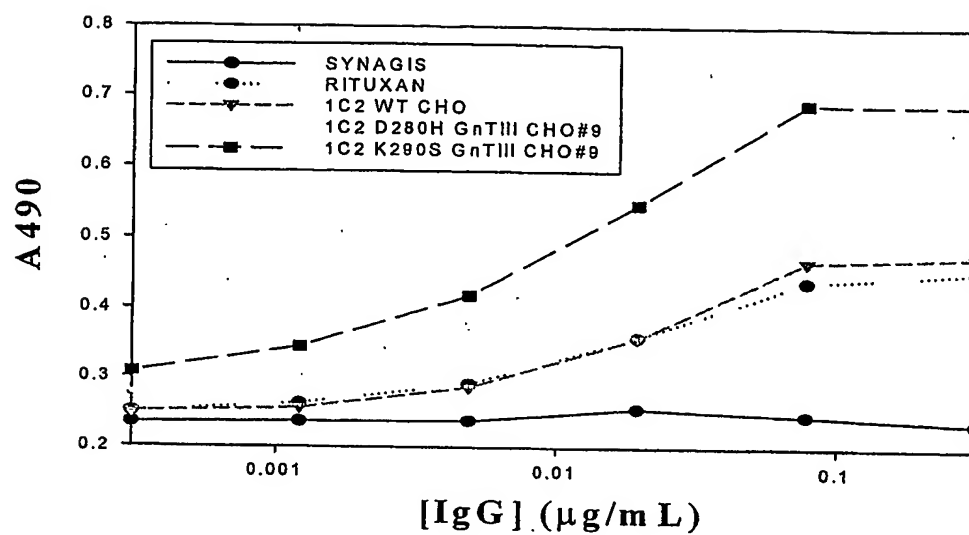


FIGURE 16



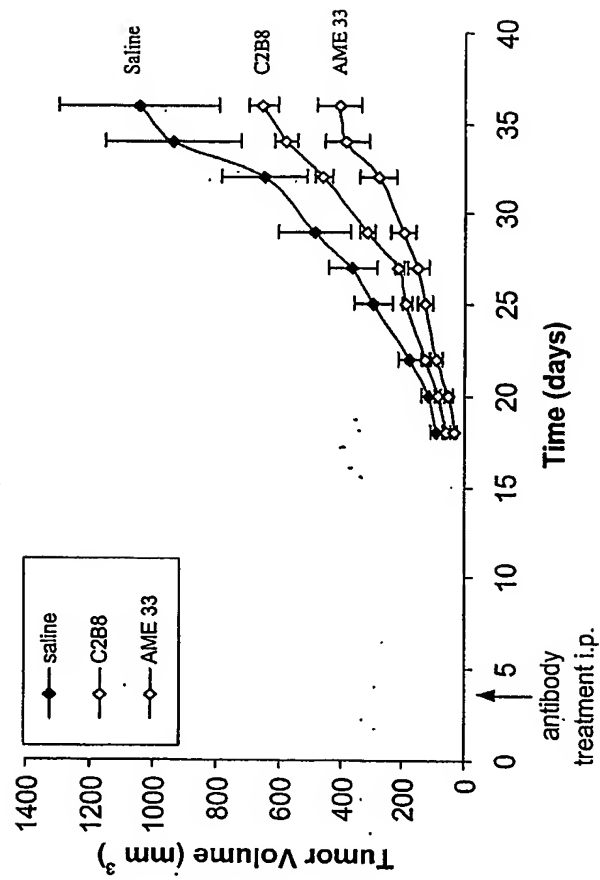


FIGURE 17

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